

FIG. 1

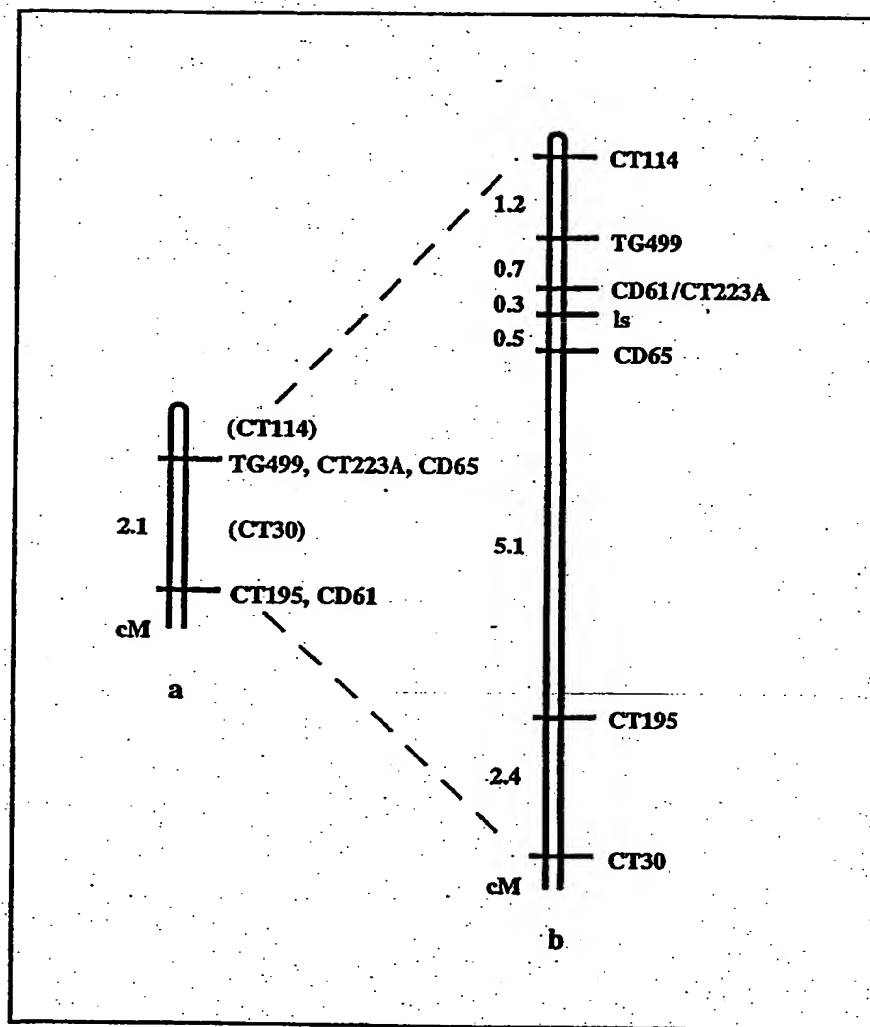


FIG. 2

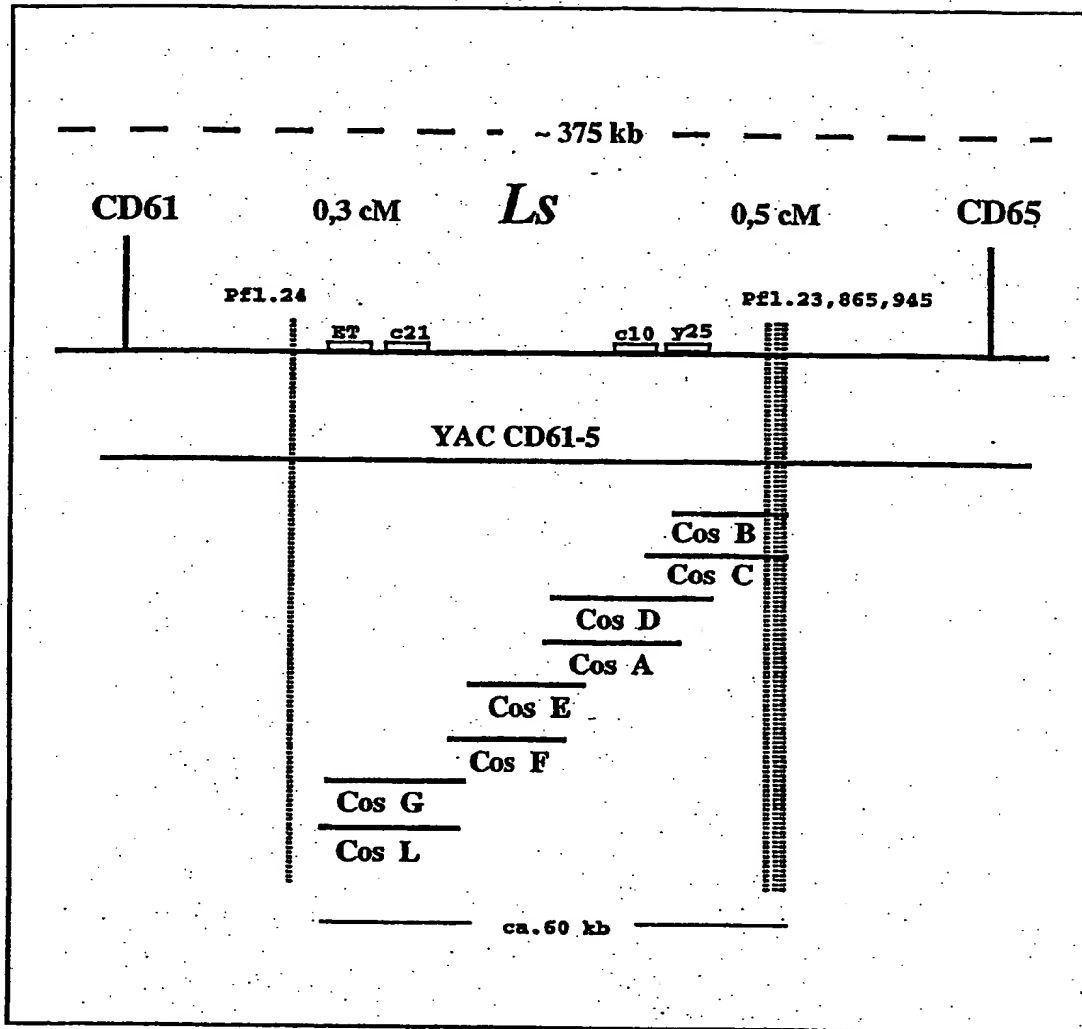


FIG. 3

A. majus  
S. tuberosum  
L. esculentum

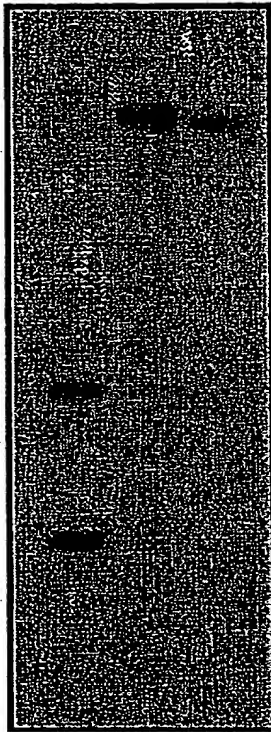


FIG. 4



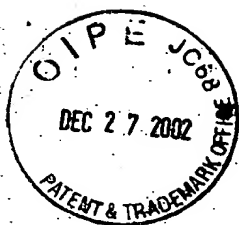
1 CCTCTGTCTCTCCCCCAGGTCCCTTTTTCCTTTCTCTCTCTCTCTTTTATTTCTCTTT 60  
61 TCATAAGCATATTCTTTCTCTCTCTAGGGTTTTTCACTTTTCACCTGAAATAGTGTGTAA 120  
121 ATTGAATGATATGTTAGGATCCTTTTGGTTCCTCATCATCTCAATCTCACCCCTCATCATGA 180  
M L G S F G S S S S Q S H P H H D  
181 TGAAGAATCTTCTGATCATCATCAACAGCGTAGATTACCGCTACTGCTACAACATATCAC 240  
E E S S D H H Q Q R R F T A T A T T I T  
241 CACCACCACCATCACTACCTCACCAGCTATTCAAATCGCCAGCTACTCATTAGCTGTGC 300  
T T T I T T S P A I Q I R Q L L I S C A  
301 GGAGTTGATTTTCGAGTCCGATTTTCTCGGCCGCGAAAAGACTCCTTACTATATTATCAAC 360  
E L I S Q S D F S A A K R L L T I L S T  
361 TAACTCATCTCCTTTTGGTGATTCAACTGAACGGTTAGTCCATCAATTTACTCGGCACT 420  
N S S P F G D S T E R L V H Q F T R A L  
421 TTCCCTTCGTCTCAACCGCTATATATCGTCAACCACCAATCATTTCATGACACCTGTGA 480  
S L R L N R Y I S S T T N H F M T P V E  
481 AACAACTCCAACGTATTCTTCTCTTCGTTCATCATTAGCTCTAATTCAATCATCATATCT 540  
T T P T D S S S S S S L A L I Q S S Y L  
541 ATCTCTAAACCAAGTTACCCCTTTTCATAAGGTTTACTCAATTAACCGCTAATCAAGCGAT 600  
S L N Q V T P F I R F T Q L T A N Q A I  
601 TTTAGAAGCGATTAAACGGTAATCATCAAGCAATCCACATCGTTGATTTGACATTAAATCA 660  
L E A I N G N H Q A I H I V D F D I N H  
661 CGGGGTTCAATGGCCACCGTTAATGCAAGCACTAGCTGATCGTTACCCCTGCTCCCACTCT 720  
G V Q W P P L M Q A L A D R Y P A P T L  
721 TCGAATCACCGGTACTGGAAATGACCTTGATACCCCTTCGTAGAACAGGTGATCGTTTAGC 780  
R I T G T G N D L D T L R R T G D R L A  
781 TAAATTTGCTCACTCATTAGGGTTGAGATTTCAATTCCATCCTCTTTATATAGCCAATAA 840  
K F A H S L G L R F Q F H P L Y I A N N  
841 TAACCACGATCAGATGAAGATCCTTCTATTATTTCTCCATTGTACTACTCCCTGATGA 900  
N H D H D E D P S I I S S I V L L P D E  
901 AACCTAGCTATCAACTGTGTTTTCTACCTCCACCGCTTTTAAAGACCGCGAAAAGTT 960  
T L A I N C V F Y L H R L L K D R E K L  
961 AAGGATTTTTTTGTCATAGGGTTAAGTCAATGAACCTAAAATTGTTACAATCGCGGAGAA 1020  
R I F L H R V K S M N P K I V T I A E K  
1021 GGAAGCAAATCATAACCATCCTCTTTTTTTTACAAAGATTCATCGAGGCGTTGGATTATTA 1080

FIG.5A



E A N H N H P L F L Q R F I E A L D Y Y  
1081 TACAGCTGTGTTTGATTCACTGGAAGCTACATTGCCACCGGGTAGTCGAGAGAGGATGAC 1140  
T A V F D S L E A T L P P G S R E R M T  
1141 AGTTGAACAAGTGTGGTTTGGGAGAGAGATTGTTGATATCGTTGCGATGGAAGGAGATAA 1200  
V E Q V W F G R E I V D I V A M E G D K  
1201 AAGGAAAGAAAGACATGAAAGGTTTAGATCATGGGAAGTTATGTTGAGGAGTTGTGGATT 1260  
R K E R H E R F R S W E V M L R S C G F  
1261 TAGTAATGTGCTTTAAGCCCTTTTGCATTATCACAAGCTAAGCTTCTTTTGAGACTTCA 1320  
S N V A L S P F A L S Q A K L L L R L H  
1321 TTATCCTTCTGAAGGCTATCAACTCGGAGTTTCGAGTAATTCCTTCTTCTTAGGTTGGCA 1380  
Y P S E G Y Q L G V S S N S F F L G W Q  
1381 AAATCAACCCCTTTTCTCCATCTCGTCTTGGCGTTGAGAAAACTATCAAATAGCCCACT 1440  
N Q P L F S I S S W R  
1441 TCAGAGGGTAATTAAGACTACTGATAGTTTAGGAGGGATCTGAAGAAAACGGCTGGAGTG 1500  
1501 AAAACCCCTAAATAACCAGATTTTCTAATGAAGTTGTAGTAGTAGAAATTTGCATGGTGAA 1560  
1561 GAACAATATTGAAGAGGTATTGAAATTTTCATGTTTTTTTGTCTTACTTATTGATATGAA 1620  
1621 TGTTTTAAAATTTTAAACATAGAGGACTAGGTTGATGATATATAGTATTTAAGTTAACTA 1680  
1681 GTCTTTGTATAACGCAAGATCTTGATCAACTTATTTTTATTTTAAATTA 1729

FIG. 5B



1 ATGTTAGGATCCTTTGGTTCTTCATCATCTCAATCTCACCTCATCATGATGAAGAATCT 60  
1 M L G S F G S S S S Q S H P H H D E E S 20  
61 TCTGATCATCATCAACGGCGTAGATTCACCGCTACTACTACAACATCACCACCACCACC 120  
21 S D H H Q R R R F T A T T T T I T T T T 40  
121 ACAACGACCTCACCAGCTATTCAAATCCGCCAGCTACTCATTAGCTGTGCGGAGTTGATT 180  
41 T T T S P A I Q I R Q L L I S C A E L I 60  
181 TCGCGTCCGATTCTCGGCCGCGAAAAGACTCCTTACCATATTATCAACTAATCTTCT 240  
61 S R S D F S A A K R L L T I L S T N S S 80  
241 CCTTTGGTGATTCAACTGAACGGTTAGTCCATCAGTTTACTCGCGCACTTTCCCTTCGT 300  
81 P F G D S T E R L V H Q F T R A L S L R 100  
301 CTCAACCGCTATATATCGTCAACCACCAATCATTTTCATGACACCTGTTGAAACAACCTCCA 360  
101 L N R Y I S S T T N H F M T P V E T T P 120  
361 ACTGATTCTTCATCTTCGTTGCCATCGTCATCATTAGCTCTAATTCAATCATCATATCAT 420  
121 T D S S S S L P S S S L A L I Q S S Y H 140  
421 TCTCTAAATCAAGTTACCCCTTTTATAAGGTTTACTCAATTAACCGCTAATCAAGCGATT 480  
141 S L N Q V T P F I R F T Q L T A N Q A I 160  
481 TTAGAAGCGATTAAACGGTAATCATCAAGCAATCCACATCGTTGATTTCGACATTAATCAC 540  
161 L E A I N G N H Q A I H I V D F D I N H 180  
541 GGGGTTCAATGGCCACCGTTAATGCAAGCACTAGCTGATCGTTACCCTGCTCCTACTCTT 600  
181 G V Q W P P L M Q A L A D R Y P A P T L 200  
601 CGAATCACCGGTACTGGAAATGACCTTGATACCTTCGTAGAACAGGTGATCGTTTAGCT 660  
201 R I T G T G N D L D T L R R T G D R L A 220  
661 AAATTGCTCACTCATTAGGGTTGAGATTTCAATTCATCCTCTTTATATCGCCAATAAT 720  
221 K F A H S L G L R F Q F H P L Y I A N N 240  
721 AACCGCGATCACGGTGAAGATCCTTCTATTATTTCTCCATTGTACTTCTCCCTGATGAA 780  
241 N R D H G E D P S I I S S I V L L P D E 260  
781 ACCCTAGCTATCAACTGTGTTTCTATCTCCACCGCCTTTTAAAAGACCGCGAAAAATTA 840  
261 T L A I N C V F Y L H R L L K D R E K L 280

FIG. 6A



841 AGGATTTTTTGCATAGGGTTAAGTCAATGAACCCTAAAATTGTTACAATCGCGGAGAAG 900  
281 R I F L H R V K S M N P K I V T I A E K 300  
901 GAAGCAAATCATAACCATCCTCTTTTTTACAAAGATTTATCGAGGCGTTGGATTATTAT 960  
301 E A N H N H P L F L Q R F I E A L D Y Y 320  
961 ACAGCTGTGTTTGATTCAATTGGAAGCTACATTGCCACCGGTAGTCGTGAGAGGATGACA 1020  
321 T A V F D S L E A T L P P G S R E R M T 340  
1021 GTTGAACAAGTGTGGTTTGGGAGAGAAATTGTTGATATCGTGGCGATGGAAGGAGATAAA 1080  
341 V E Q V W F G R E I V D I V A M E G D K 360  
1081 AGGAAAGAAAGACATGAAAGGTTTAGATCATGGGAAGTTATGTTGAGGAGTTGTGGATTT 1140  
361 R K E R H E R F R S W E V M L R S C G F 380  
1141 AGTAATGTTGCTTTAAGCCCTTTTGCATTATCACAAGCTAAGCTTCTTTTGAGACTACAT 1200  
381 S N V A L S P F A L S Q A K L L L R L H 400  
1201 TATCCTTCTGAAGGCTATCAACTCGGAGTTTCGAGTAATTCTTTCTTCTTAGGTTGGCAA 1260  
401 Y P S E G Y Q L G V S S N S F F L G W Q 420  
1261 AATCAACCTCTTTTCTCCATCTCGTCTTGGCGTTGA 1296  
421 N Q P L F S I S S W R \* 432

FIG. 6B





1 GAGAGGTCATCAAACCCTAGCAGTCCACCTCCATCTCTCCGCATAACCGGATGCGGTCTGA 60  
E R S S N P S S P P P S L R I T G C G R  
61 GATGTAACCGGATTAAACCGAACTGGAGACCGTTAACCCGGTTCGCTGACTCTTTAGGT 120  
D V T G L N R T G D R L T R F A D S L G  
121 CTCCAATTCCAGTTTCACACGCTAGTGATCGTAGAAGAAGATCTCGCCGGACTTTTGCTA 180  
L Q F Q F H T L V I V E E D L A G L L L  
181 CAGATCCGATTGTTAGCTCTCTCAGCCGTACAAGGAGAGACCATTGCCGTCAATTGTGTT 240  
Q I R L L A L S A V Q G E T I A V N C V  
241 CACTTCCTCCACAAAATATTTAAGCAGATGGAGATATGATCGGTCACTTCTTGTCAGCG 300  
H F L H K I F N D D G D M I G H F L S A  
301 ATCAAGAGCTTAAACTCTAGAATCGTTACAATGGCAGAGAGAGAAGCTAATCATGGAGAT 360  
I K S L N S R I V T M A E R E A N H G D  
361 CACTCGTTCTTGAATAGATTCTCTGAGGCAGTGGATCATTACATGGCGATCTTTGATTCTG 420  
H S F L N R F S E A V D H Y M A I F D S  
421 TTGGAAGCGACGTTGCCGCCAAATAGCCGAGAGAGACTAACCCTAGAGCAACGGTGGTTCT 480  
L E A T L P P N S R E R L T L E Q R W F  
481 GGTAAGGAGATTTTGGATGTTGTGGCGCGGAAGAGACGGAGAGAAAGCAAAGACATCGG 540  
G K E I L D V V A A E E T E R K Q R H R  
541 AGGTTTGAGATTTGGGAAGAGATGATGAAGAGGTTTGGTTTCGTTAACGTTCTTATTGGA 600  
R F E I W E E M M K R F G F V N V P I G  
601 AGCTTTGCTTTGTCTCAAGCTAAGCTTCTTCTTAGACTTCATTATCCTTCAGAAGGTTAT 660  
S F A L S Q A K L L L R L H Y P S E G Y  
661 AATCTTCAGTTCCTTAACAATTCTTTG 687  
N L Q F L N N S L

FIG. 7

LSAt	1	ALGSFGSSSSQSHPHHDEESSDDHQQRRFTATTTT	TTTSPAIQIRQLLISCAELI
LSLe	1	ALGSFGSSSSQSHPHHDEESSDDHQQRRFTATTTT	TTTSPAIQIRQLLISCAELI
LSSt	1	ALGSFGSSSSQSHPHHDEESSDDHQQRRFTATTTT	TTTSPAIQIRQLLISCAELI
LSAt	1	5DFSAAKRLLTILSTNSSPFGDSTERLVHQFTRALSRLNRYSSTTNHFMTPVETTP	
LSLe	61	5DFSAAKRLLTILSTNSSPFGDSTERLVHQFTRALSRLNRYSSTTNHFMTPVETTP	
LSSt	61	5DFSAAKRLLTILSTNSSPFGDSTERLVHQFTRALSRLNRYSSTTNHFMTPVETTP	
LSAt	1	TDSSSSSSSLALIQSSYSLNQVTPFIRFTOLTANQAILAINGNHQAIHIVDFDINH	
LSLe	121	TDSSSSSSSLALIQSSYSLNQVTPFIRFTOLTANQAILAINGNHQAIHIVDFDINH	
LSSt	121	TDSSSSSSSLALIQSSYSLNQVTPFIRFTOLTANQAILAINGNHQAIHIVDFDINH	
LSAt	1	ERSSNPSSPPPLRITGCGRDTGRTGDRRLTFA5LGLQFQFHTLIVVEE	
LSLe	178	GVQWPPPLMOALADRYPAPTLLRITGCGNDLDTLRRTCDDLAKFAHSLGLRFQFHPLYIANN	
LSSt	181	GVQWPPPLMOALADRYPAPTLLRITGCGNDLDTLRRTCDDLAKFAHSLGLRFQFHPLYIANN	
LSAt	54	DLAQLLQIRLALBAVQGETANCVHLLHNDDEMIGHFLSAKSNELVTIAE	
LSLe	238	NDDHDEDPSIISSIVLLPDETLAINCVFYHLRLLK.DREKLRIFLHRVKSMNPKIVTIAE	
LSSt	241	NDDHDEDPSIISSIVLLPDETLAINCVFYHLRLLK.DREKLRIFLHRVKSMNPKIVTIAE	
LSAt	114	KEANHGDHSFLRFSEA D HMAFDSLEATLPPYERERTEQRWFGETIDVALEET	
LSLe	297	KEANHNNHPLFLQRFIEALDY YTAVFDSLEATLPPGSRERMTVEQVWFGREIIVDIVAMEGD	
LSSt	300	KEANHNNHPLFLQRFIEALDY YTAVFDSLEATLPPGSRERMTVEQVWFGREIIVDIVAMEGD	
LSAt	174	ERKRRHRRFIIEEELRFFVNVFCSFALSQAKLLRLRLHYPSEGYLFLNNS	
LSLe	357	KRKRHERFRSWEVMLRSCGFSNVALSPFALSOAKLLRLRLHYPSEGYQLGVSSNSFFLGGW	
LSSt	360	KRKRHERFRSWEVMLRSCGFSNVALSPFALSOAKLLRLRLHYPSEGYQLGVSSNSFFLGGW	
LSAt	230	DNQPLFSISSWR	
LSLe	417	DNQPLFSISSWR	
LSSt	420	DNQPLFSISSWR	

FIG. 8